STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 182414

TO: Sheela Huff
Location: rem/3A15/3C18
Art Unit: 1643
Friday, March 17, 2006
Case Serial Number: 10/609217

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

RUSH

STIC-Biotech/ChemLib 182414

From: Huff, Sheela
Sent: Tuesday, February 21, 2006 6:44 AM
To: STIC-Biotech/ChemLib
Subject: search request for 10/609217

Please search and interference search SEQ ID NO. 2.

thanks-

Sheela Huff
Art Unit 1643
571-272-0834
Remsen 3A15
mailbox Remsen 3C18

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 16, 2006, 19:57:23 ; Search time 191 Seconds
(without alignments)
524.494 Million cell updates/sec

Title: US-10-609-217-2
Perfect score: 1238
Sequence: 1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1238	100.0	228	3	AAY96529	Aay96529 Human IgG
2	1238	100.0	228	3	AAB16955	Aab16955 Human IgG
3	1238	100.0	228	4	AAB98953	Aab98953 Human IgG
4	1238	100.0	228	5	ABB04279	Abb04279 Human IgG
5	1238	100.0	228	5	AAU81074	Aau81074 Human IgG
6	1238	100.0	228	5	AAE14310	Aae14310 Human imm
7	1238	100.0	228	5	ABB73410	Abb73410 Human imm
8	1238	100.0	228	5	AAG66012	Aag66012 Human imm
9	1238	100.0	228	5	AAU73018	Aau73018 Human imm
10	1238	100.0	228	6	ABJ38267	Abj38267 Human IgG
11	1238	100.0	228	7	ADN59683	Adn59683 Human IgG
12	1238	100.0	228	8	ADM17708	Adm17708 Human IgG
13	1238	100.0	228	8	ADQ75329	Adq75329 Human IgG
14	1238	100.0	243	3	AAB17957	Aab17957 Fc-MMP in
15	1238	100.0	243	5	ABB73425	Abb73425 Fc-MMP in
16	1238	100.0	243	7	ADN59746	Adn59746 Vector 20
17	1238	100.0	247	3	AAB16958	Aab16958 Fc-TMP pr
18	1238	100.0	247	5	ABB73411	Abb73411 Fc-TPO mi
19	1238	100.0	248	3	AAB17951	Aab17951 Fc-TNF-al
20	1238	100.0	248	3	AAB17953	Aab17953 Fc-IL-1 a
21	1238	100.0	248	5	ABB73421	Abb73421 Fc-interl
22	1238	100.0	248	5	ABB73419	Abb73419 Fc-TNF-al
23	1238	100.0	250	7	ADD31616	Add31616 Ang-2 pep
24	1238	100.0	250	8	ADT71978	Adt71978 Ang-2 neg
25	1238	100.0	252	3	AAB17955	Aab17955 Fc-VEGF a
26	1238	100.0	252	5	ABB73423	Abb73423 Fc-VEGF a
27	1238	100.0	253	3	AAB16964	Aab16964 Fc-EMP pr
28	1238	100.0	253	5	ABB73415	Abb73415 Fc-EPO mi
29	1238	100.0	259	9	AEA18572	Aea18572 Amino aci
30	1238	100.0	268	3	AAB16959	Aab16959 Fc-TMP-TM
31	1238	100.0	268	5	ABB73412	Abb73412 Fc-TMP-TM
32	1238	100.0	269	3	AAY96531	Aay96531 Human IgG
33	1238	100.0	277	3	AAB16967	Aab16967 Fc-EMP-EM
34	1238	100.0	277	5	ABB73418	Abb73418 Fc-EMP-EM
35	1238	100.0	282	5	AAU81169	Aau81169 Echistati
36	1238	100.0	374	2	AAW49075	Aaw49075 Recombina
37	1238	100.0	374	2	AAW83963	Aaw83963 Recombina
38	1238	100.0	374	9	AEB51285	Aeb51285 Recombina
39	1238	100.0	401	4	AAB80904	Aab80904 Human met
40	1238	100.0	401	4	AAY72922	Aay72922 Human met
41	1235	99.8	406	7	ADP75162	Adp75162 Fusion co
42	1235	99.8	409	7	ADP75170	Adp75170 Fusion co
43	1235	99.8	409	7	ADP75176	Adp75176 Fusion co
44	1235	99.8	410	7	ADP75166	Adp75166 Fusion co
45	1235	99.8	412	7	ADP75168	Adp75168 Fusion co

ALIGNMENTS

RESULT 1
AAY96529
ID AAY96529 standard; protein; 228 AA.
XX
AC AAY96529;
XX
DT 04-SEP-2000 (first entry)
XX
DE Human IgG1 Fc chain.
XX
KW Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet;
KW megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV;
KW anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
XX
OS Homo sapiens.
XX
PN WO200024770-A2.
XX
PD 04-MAY-2000.
XX
PF 22-OCT-1999; 99WO-US024834.
XX
PR 23-OCT-1998; 98US-0105348P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Liu C, Feige U, Cheetham J;
XX
DR WPI; 2000-365108/31.
DR N-PSDB; AAA29220.
XX
PT Thrombopoietic peptides which activate mpl receptors and increase the
PT production of platelets or platelet precursors, useful for treatment of
PT diseases which involve thombocytopenia.
XX
PS Disclosure; Page 76-77; 91pp; English.
XX
CC A compound which binds to an mpl receptor comprising a thrombopoietin
CC mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is
CC new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to
CC 14 residues in length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2, X_2-
CC X_1_3, X_2-X_1_4, X_1-X_1_0, X_1-X_1_1, X_1-X_1_2, X_1-X_1_3, and X_1-
CC X_1_4. X_1 = I, A, V, L, S or R; X_2 = E, D, K or V; X_3 = G or A; X_4 =
CC P; X_5 = T or S; X_6 = L, I, V, A or F; X_7 = R or K; X_8 = Q, N, or E;
CC X_9 = W, Y or F; X_1_0 = L, I, V, A, F, M, or K; X_1_1 = A, I, V, L, F,
CC S, T, K, H, or E; X_1_2 = A, I, V, L, F, G, S, or Q; X_1_3 = R, K, T, V,
CC N, Q or G; X_1_4 = A, I, V, L, F, T, R, E, or G; L_1 = linker comprising

CC 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate
CC the c-Mpl receptor which mediates the activity of endogenous
CC thrombopoietin. The TMPs are useful for increasing the production of
CC platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which
CC is useful for treatment of diseases which involve thombocytopenia, e.g.
CC aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
CC virus associated ITP, and systemic lupus erythematosus
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 3; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

RESULT 2
AAB16955
ID AAB16955 standard; protein; 228 AA.
XX
AC AAB16955;
XX
DT 31-OCT-2000 (first entry)
XX
DE Human IgG1 Fc protein sequence SEQ ID NO:2.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
XX
OS Homo sapiens.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
DR N-PSDB; AAA69443.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Claim 7; Page 176-177; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 3; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

RESULT 3
AAB98953
ID AAB98953 standard; protein; 228 AA.
XX
AC AAB98953;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human IgG1 Fc region.
XX
KW Human; IgG1; immunoglobulin; Fc region; Fc fusion protein; misfolding;
KW therapy; cancer; osteoarthritis; AIDS; obesity; inflammation;
KW transplant rejection.
XX
OS Homo sapiens.
XX
PN WO200134638-A1.
XX
PD 17-MAY-2001.
XX
PF 10-NOV-2000; 2000WO-US030798.
XX
PR 12-NOV-1999; 99US-0165188P.
PR 09-NOV-2000; 2000US-00709704.
XX
PA (AMGE-) AMGEN INC.
XX
PI Treuheit MJ, O'conner SR, Kosky AA;
XX
DR WPI; 2001-335908/35.
DR N-PSDB; AAH25762.
XX

PT Correcting disulfide bond misfolds in Fc-containing proteins,
PT particularly therapeutic Fc-containing fusion proteins or antibodies, by
PT treatment with copper halide.
XX
PS Claim 30; Fig 5; 59pp; English.
XX
CC The present invention describes a process for preparing a
CC pharmacologically active compound, involving preparing a compound
CC comprising an immunoglobulin Fc domain fused to a protein of interest,
CC treating the compound with a copper(II) halide and isolating the treated
CC molecule. This can be used to correct misfolding of Fc domain containing
CC proteins, for use in therapeutic agents which may be used in the
CC treatment of cancer, inflammation, transplant rejection, AIDS,
CC osteoarthritis and obesity. The present sequence is the IgG1 Fc domain
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

RESULT 4
ABB04279
ID ABB04279 standard; protein; 228 AA.
XX
AC ABB04279;
XX
DT 13-FEB-2002 (first entry)
XX
DE Human IgG1 Fc domain.
XX
KW Glucagon antagonist; antidiabetic; anti-hormonal; Fc domain;
KW non-insulin dependent diabetes mellitus; human; immunoglobulin G; IgG.
XX
OS Homo sapiens.
XX
PN WO200183527-A2.
XX
PD 08-NOV-2001.
XX
PF 03-MAY-2001; 2001WO-US014321.
XX
PR 03-MAY-2000; 2000US-0201436P.
PR 02-MAY-2001; 2001US-00847249.
XX
PA (AMGE-) AMGEN INC.
XX
PI Marshall WS, Stark KL;
XX
DR WPI; 2002-017738/02.
DR N-PSDB; ABA03672.
XX
PT Compositions comprising glucagon antagonist domains, useful for treating
PT diabetes mellitus.
XX
PS Claim 8; Fig 2; 54pp; English.
XX
CC The invention relates to compositions comprising a glucagon antagonist
CC domain and a vehicle, such as a polymer (e.g. PEG or dextran) or,
CC preferably, an Fc domain. The vehicle is covalently attached to the
CC glucagon antagonist domain. The compositions are administered to treat
CC non-insulin dependent diabetes mellitus. The present sequence is the
CC human IgG Fc domain, which may be used as the vehicle in the compositions
CC of the invention
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

RESULT 5
AAU81074
ID AAU81074 standard; protein; 228 AA.
XX
AC AAU81074;
XX
DT 09-APR-2002 (first entry)
XX
DE Human IgG1 Fc.
XX
KW Human; IgG Fc; anticoagulant; thrombolytic; cytostatic; antiinflammatory;
KW immunosuppressive; osteopathic; antagonist; laminin; saw-scaled viper;
KW echistatin; integrin; selectin; vinculin; platelet aggregation;
KW angiogenesis; tumour; inflammation; autoimmune disease;
KW rheumatoid arthritis; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200181377-A2.
XX
PD 01-NOV-2001.
XX
PF 23-APR-2001; 2001WO-US013069.
XX
PR 21-APR-2000; 2000US-0198919P.
PR 03-MAY-2000; 2000US-0201394P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Kohno T, Lacey DL, Boone TC;
XX
DR WPI; 2002-062025/08.
DR N-PSDB; ABK24097.
XX
PT Composition comprising integrin or adhesion antagonistic peptide and
PT vehicle, useful for treating or preventing platelet aggregation, has a
PT longer half-life than free peptide.
XX
PS Claim 9; Fig 3; 68pp; English.
XX
CC The invention relates to a composition comprising an integrin/adhesion

```
CC   antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are
CC   based on laminin or saw-scaled viper echistatin and target integrin,
CC   selectin or vinculin.Also included are compounds of formula (Ia) and
CC   their multimers (X^1)_a-P^1-(X^2)_b where; P^1 = Fc domain; X^1 and X^2 =
CC   -(L^1)_c-P^1, (L^1)_c-P^1-(L^2)_d-P^2, (L^1)_c-P^1-(L^2)_d-P^2-(L^3)_e-
CC   P^3 or (L^1)_c-P^1-(L^2)_d-P^2-(L^3)_e-P^3-(L^4)_f-P^4; P^1-P^4 = same or
CC   different (I); L^1-L^4 = same or different linkers; a-f = 0 or 1,
CC   provided at least one of a and b = 1, a nucleic acid that encodes (Ia),
CC   an expression vector containing the nucleic acid, host cells containing
CC   the vector, producing a pharmaceutically active compound (B) by
CC   covalently linking at least one Fc domain to at least one amino acid
CC   sequence of a selected randomized (I) and any of six laminin-related
CC   peptides (Ib). The compositions are used prophylactically and
CC   therapeutically in the same way as (I), e.g. to inhibit platelet
CC   aggregation or angiogenesis (tumours), or to treat inflammation and
CC   autoimmune diseases (e.g. rheumatoid arthritis) and many different forms
CC   of osteoporosis, also for diagnosis. Attaching the vehicle (especially Fc
CC   domain) to (I) increases the half-life (free (I) are normally degraded
CC   very quickly in vivo). The present sequence is human IgG1 Fc which is
CC   used as a vehicle for the antagonists of the invention
XX
SQ   Sequence 228 AA;

  Query Match             100.0%;  Score 1238;  DB 5;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-90;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 6
AAE14310
ID   AAE14310 standard; protein; 228 AA.
XX
AC   AAE14310;
XX
DT   07-MAR-2002  (first entry)
XX
DE   Human immunoglobulin G (IgG1) Fc.
XX
KW   Human; calcitonin; CT; CT receptor; Fc domain; therapy; osteoporosis;
KW   immunoglobulin G; IgG; osteopathic.
XX
OS   Homo sapiens.
XX
PN   WO200183526-A2.
XX
PD   08-NOV-2001.
XX
PF   03-MAY-2001; 2001WO-US014320.
XX
PR   03-MAY-2000; 2000US-0201511P.
PR   02-MAY-2001; 2001US-00847712.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Liu C,  Marshall WS,  Reynolds A;
XX
DR   WPI; 2002-034503/04.
DR   N-PSDB; AAD23840.
XX
PT   Compositions comprising Calcitonin receptor modulator domains, useful for
PT   treating osteoporosis.
XX
PS   Claim 8; Fig 3; 64pp; English.
XX
CC   The invention relates to therapeutic agents that modulate the activity of
CC   calcitonin (CT) receptor. Modulators of CT receptor comprise a CT
CC   receptor modulating domain and a vehicle such as a polymer or an Fc
CC   domain, where the vehicle is covalently attached to the CT receptor
CC   modulating domain. The compositions comprising CT receptor modulating
CC   domains are used to treat osteoporosis. The present sequence is human
CC   immunoglobulin G (IgG1) Fc protein used in the invention
XX
SQ   Sequence 228 AA;

  Query Match             100.0%;  Score 1238;  DB 5;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-90;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 7
ABB73410
ID   ABB73410 standard; protein; 228 AA.
XX
AC   ABB73410;
XX
DT   05-APR-2002  (first entry)
XX
DE   Human immunoglobulin G1 Fc (IgG1 Fc) amino acid SEQ ID NO:2.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
```

PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
DR N-PSDB; ABL35760.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS Claim 7; Fig 4; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

RESULT 8
AAG66012
ID AAG66012 standard; protein; 228 AA.
XX
AC AAG66012;
XX
DT 27-FEB-2002 (first entry)
XX
DE Human immunoglobulin (Ig) G1 Fc region sequence.
XX
KW Apo-AI; amphipathic; pharmaceutical; peptide mimic; antilipemic;
KW anti-HIV; virucide; immunoglobulin; IgG1.
XX
OS Homo sapiens.
XX
PN WO200181376-A2.
XX
PD 01-NOV-2001.
XX
PF 23-APR-2001; 2001WO-US013068.
XX
PR 21-APR-2000; 2000US-0198920P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Kohno T;
XX
DR WPI; 2002-049262/06.
DR N-PSDB; AAI67658.
XX
PT Recombinant or modified therapeutic agents having Apo-AI amphipathic
PT helix peptide activity useful in treatment of hypercholesterolemia and
PT viral infections such as herpes simplex virus, human immunodeficiency
PT virus.
XX
PS Claim 8; Fig 3A-B; 49pp; English.
XX
CC The invention provides a composition comprising a therapeutic agent that
CC has activity similar to Apo-AI amphipathic helix peptide, but with better
CC pharmaceutical characteristics attached to a vehicle through the
CC peptide's N-terminus or C-terminus having a specified formula. The
CC peptide mimic has greater half-life compared to conventional Apo-AI
CC amphipathic helix peptide. The compositions are useful for treating
CC hypercholesterolemia and viral infection such as HIV, HSV. The present
CC sequence represents the human immunoglobulin (Ig) G1 Fc region which acts
CC as a vehicle
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

RESULT 9
AAU73018
ID AAU73018 standard; protein; 228 AA.
XX
AC AAU73018;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human immunoglobulin G (IgG) Fc region.
XX
KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX
OS Homo sapiens.
XX
PN WO200181415-A2.
XX
PD 01-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US013528.
XX
PR 27-APR-2000; 2000US-0200053P.
PR 28-JUN-2000; 2000US-0214860P.
PR 06-FEB-2001; 2001US-0266673P.
PR 26-APR-2001; 2001US-00843221.
XX
PA (AMGE-) AMGEN INC.
XX
PI Kostenuik P, Liu C, Lacey DL;
XX
DR WPI; 2002-066435/09.
DR N-PSDB; AAS97392.
XX
PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators.
XX
PS Claim 6; Fig 3; 107pp; English.
XX
CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention
XX
SQ Sequence 228 AA;

```
  Query Match             100.0%;  Score 1238;  DB 5;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-90;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 10
ABJ38267
ID ABJ38267 standard; protein; 228 AA.

XX
AC ABJ38267;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human IgG1 Fc protein SEQ ID No 2.
XX
KW TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune disease;
KW systemic lupus erythematosus; B-cell-mediated cancer; lymphoma;
KW inflammation; rheumatoid arthritis; acute pancreatitis; atherosclerosis;
KW Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis;
KW glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis;
KW multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;
KW gene therapy; human IgG1Fc; human.
XX
OS Homo sapiens.
XX
PN WO200292620-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US015273.
XX
PR 11-MAY-2001; 2001US-0290196P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Min H, Hsu H;
XX
DR WPI; 2003-156719/15.
DR N-PSDB; ABT33856.
XX
PT New TALL-1-binding polypeptide, useful for modulating the activity of
PT TALL-1 and in treating, preventing or diagnosing a B-cell-mediated
PT autoimmune diseases, cancers or lymphomas.
XX
PS Claim 36; Fig 3; 236pp; English.
XX
CC The invention relates to a novel TALL-1-binding polypeptide comprising a
CC defined sequence in the specification. The composition is useful in
CC modulating the activity of TALL-1, and in treating, preventing,
CC ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune
CC disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or
CC lymphoma. The composition may also be used in treating inflammations
CC (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease,
CC asthma, atherosclerosis, cachexia, cirrhosis, diabetes,
CC glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple
CC myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis
CC and vasculitis. Disorders may be treated with the novel composition using
CC gene therapy. This sequence represents a human IgG1Fc protein relating to
CC the TALL-1 sequence of the invention
XX
SQ Sequence 228 AA;

```
  Query Match             100.0%;  Score 1238;  DB 6;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-90;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

```
RESULT 11
ADN59683
ID   ADN59683 standard; protein; 228 AA.
XX
AC   ADN59683;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human IgG1 Fc amino acid sequence, seq id 32.
XX
KW   Haemostatic; antianaemic; immunosuppressive; platelet;
KW   transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
KW   TMP; c-mpl receptor; platelet precursor; megakaryocyte;
KW   thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia;
KW   autoimmune haemolytic anaemia; Hughe's syndrome;
KW   lupoid thrombocytopaenia; IgG1.
XX
OS   Homo sapiens.
XX
PN   WO2003031589-A2.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032552.
XX
PR   11-OCT-2001; 2001US-0328666P.
PR   10-OCT-2002; 2002US-00269806.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Min H,  Sitney KC,  Hartley C;
XX
DR   WPI; 2003-403101/38.
DR   N-PSDB; ADN59682.
XX
PT   Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
PT   which stimulate the production of platelets and/or the production of
PT   platelet precursors, useful for treating thrombocytopenia.
XX
PS   Disclosure; SEQ ID NO 32; 126pp; English.
XX
CC   The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
CC   binds to the c-mpl (mpl) receptor, and which stimulates the production of
CC   platelets and/or the production of platelet precursors, is new. Further
CC   disclosed is a composition of matter (II) that binds to an mpl receptor,
CC   and a pharmaceutical composition comprising (II) and a carrier. The
CC   pharmaceutical composition of the invention is useful for treating
CC   thrombocytopaenia in an animal, and for increasing megakaryocytes or
CC   platelets in a patient. The TMP of the invention is useful for treating
CC   conditions involving a megakaryocyte and/or platelet deficiency, e.g.
CC   disease conditions involving thrombocytopaenia such as aplastic anaemia,
CC   autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia,
CC   autoimmune haemolytic anaemia, Hughe's syndrome and lupoid
CC   thrombocytopaenia. The TMP of the invention is also useful for
CC   maintaining the viability or storage life of platelets and/or
CC   megakaryocytes and its derived cells. The compounds demonstrate an
CC   improved ability to bind to and/or trigger transmembrane signal through,
CC   i.e. activating, the mpl receptor the compounds have superior
CC   thromobopoietic activity, i.e. the ability to stimulate, in vivo and in
CC   vitro, the production of platelets and/or megakaryocytopoietic activity,
CC   i.e. the ability to stimulate, in vivo and in vitro, the production of
CC   platelet precursors. Further, certain of the compounds also exhibit
CC   superior therapeutic properties, such as improved plasma half-life,
CC   biological activity and in vivo circulation time. The current sequence
CC   represents the human IgG1 Fc protein that may be used as a preferred
CC   vehicle of the invention.
XX
SQ   Sequence 228 AA;

  Query Match             100.0%;  Score 1238;  DB 7;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-90;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 12
ADM17708
ID   ADM17708 standard; protein; 228 AA.
XX
AC   ADM17708;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Human IgG1 Fc protein SEQ ID NO:60.
XX
KW   nerve growth factor modulator; NGF modulator; analgesic; NGF inhibitor;
KW   nerve growth factor inhibitor; neurologic pain; diabetic neuropathy;
KW   post-herpetic neuralgia; inflammatory pain; migraine; asthma;
KW   hyperactive bladder; psoriasis; cancer; acute pain; dental pain;
KW   surgical pain; pain; causalgia; demyelinating disease;
KW   trigeminal neuralgia; chronic alcoholism; stroke; thalamic pain syndrome;
KW   diabetes; acquired immuno deficiency syndrome; AIDS; headache;
KW   inflammation; arthritis; rheumatic disease; lupus; osteoarthritis;
KW   inflammatory bowel disorder; inflammatory eye disorder; sunburn;
KW   carditis; dermatitis; myositis; neuritis; collagen vascular disease;
KW   chronic inflammatory condition; neuropathic pain; genitourinary; wound;
KW   burn; allergic skin reaction; pruritus; vitiligo;
KW   gastrointestinal disorder; colitis; gastric ulceration; duodenal ulcer;
KW   human; IgG1 Fc; immunoglobulin G.
XX
OS   Homo sapiens.
XX
PN   WO2004026329-A1.
XX
PD   01-APR-2004.
XX
PF   19-SEP-2003; 2003WO-US029866.
XX
PR   19-SEP-2002; 2002US-0412524P.
PR   18-SEP-2003; 2003US-00666480.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boone TC,  Wild KD,  Sitney KC,  Min H,  Kimmel B;
XX
DR   WPI; 2004-283150/26.
DR   N-PSDB; ADM17707.
XX
PT   Novel peptide capable of modulating nerve growth factor activity, useful
PT   for treating disease or disorder e.g., acute pain, dental pain, cancer,
PT   migraine and collagen vascular disease.
XX
PS   Claim 16; SEQ ID NO 60; 267pp; English.
XX
CC   The present invention describes a peptide (I) that is capable of
CC   modulating nerve growth factor (NGF) activity. Also described: (1)
CC   modified peptide (II) comprising (I) and a vehicle, where the modified
CC   peptide is capable of modulating NGF activity; (2) dimer or multimer of
CC   (I); (3) modified peptide (III), its multimers or its salt, where the
```

```
CC   peptide is capable of modulating NGF activity; (4) polynucleotide (IV)
CC   encoding (I), (II) or (III); (5) expression vector (V) comprising (IV);
CC   (6) host cell (VI) comprising (V); (7) a composition (VII) of matter and
CC   a vehicle, where the composition of matter is capable of modulating NGF
CC   activity; and (8) pharmaceutical composition comprising (I), (II) or
CC   (III) and a diluent or carrier. (I) has analgesic activity, and can be
CC   used as an inhibitor of NGF. (I) is useful for treating or preventing a
CC   disease or disorder associated with NGF activity by administering (I) to
CC   human or animal. The disease or disorder chosen from neurologic pain,
CC   painful diabetic neuropathy, post-herpetic neuralgia, inflammatory pain,
CC   migraine, asthma, hyperactive bladder, psoriasis, cancer, acute pain,
CC   dental pain, pain from trauma, surgical pain, pain resulting from
CC   amputation or abscess, causalgia, demyelinating diseases, trigeminal
CC   neuralgia, chronic alcoholism, stroke, thalamic pain syndrome, diabetes,
CC   acquired immuno deficiency syndrome (AIDS), toxins and chemotherapy,
CC   general headache, cluster headache, mixed-vascular and non-vascular
CC   syndromes, tension headache, general inflammation, arthritis, rheumatic
CC   diseases, lupus, osteoarthritis, inflammatory bowel disorders,
CC   inflammatory eye disorders, inflammatory or unstable bladder disorders,
CC   skin complaints with inflammatory components, sunburn, carditis,
CC   dermatitis, myositis, neuritis, collagen vascular diseases, chronic
CC   inflammatory conditions, inflammatory pain associated hyperalgesia and
CC   allodynia, neuropathic pain and associated hyperalgesia and allodynia,
CC   diabetic neuropathy pain, sympathetically maintained pain,
CC   deafferentation syndromes, epithelial tissue damage or dysfunction,
CC   herpes simplex, post-herpetic neuralgia, disturbances of visceral
CC   motility at respiratory, genitourinary, gastrointestinal or vascular
CC   regions, wounds, burns, allergic skin reactions, pruritus, vitiligo,
CC   general gastrointestinal disorders, colitis, gastric ulceration, duodenal
CC   ulcers, vasomotor or allergic rhinitis, or bronchial disorders. (I) is
CC   also useful for modulating pain or promoting analgesia by administering
CC   (I) to human or animal. (I) is also useful in the manufacture of
CC   medicament for the treatment of disease or disorder. The present sequence
CC   is used in the exemplification of the present invention.
XX
SQ   Sequence 228 AA;

  Query Match             100.0%;  Score 1238;  DB 8;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-90;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 13
ADQ75329
ID   ADQ75329 standard; protein; 228 AA.
XX
AC   ADQ75329;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Human IgG1 Fc protein.
XX
KW   parathyroid hormone; parathyroid hormone-related protein; PTH; PTHrP;
KW   osteopathic; osteopenia; IgG Fc; antibody.
XX
OS   Homo sapiens.
XX
PN   WO2004060386-A1.
XX
PD   22-JUL-2004.
XX
PF   01-NOV-2002; 2002WO-US036419.
XX
PR   01-NOV-2002; 2002WO-US036419.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Kostenuik P,  Gegg CV,  Jarosinski MA,  Kinstler OB;
XX
DR   WPI; 2004-543796/52.
XX
PT   New composition of matter comprising parathyroid hormone/parathyroid
PT   hormone-related protein (PTH/PTHrP) modulating domain and a vehicle, or
PT   its multimers, useful for treating osteopenia.
XX
PS   Disclosure; Fig 3A-C; 132pp; English.
XX
CC   The invention relates to a composition comprising the formula (I): (I) P1
CC   -(L1)a-F1, where F1 = a vehicle and is attached at the C-terminus of P1-
CC   (L1)a or through a sidechain at any residue from residue 14 through the C
CC   -terminal residue; P1 = a parathyroid hormone/parathyroid hormone-related
CC   protein (PTH/PTHrP) modulating domain; L1 is a linker; and a = 0 or 1.
CC   The composition of matter is useful for treating osteopenia. This
CC   sequence corresponds to a human IgG Fc used in the invention.
XX
SQ   Sequence 228 AA;

  Query Match             100.0%;  Score 1238;  DB 8;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-90;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228


RESULT 14
AAB17957
ID   AAB17957 standard; protein; 243 AA.
XX
AC   AAB17957;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Fc-MMP inhibitor fusion protein sequence SEQ ID NO:1068.
XX
KW   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW   immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW   inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW   cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW   vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW   thrombosis; pharmaceutical.
XX
OS   Synthetic.
XX
PN   WO200024782-A2.
XX
```

PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
DR N-PSDB; AAA69507.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Example 7; Page 585-586; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 1238; DB 3; Length 243;
Best Local Similarity 100.0%; Pred. No. 5e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

RESULT 15
ABB73425
ID ABB73425 standard; protein; 243 AA.
XX
AC ABB73425;
XX
DT 05-APR-2002 (first entry)
XX
DE Fc-MMP inhibitor fusion nucleic acid SEQ ID NO:1067.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014310.
XX
PR 03-MAY-2000; 2000US-00563286.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
DR N-PSDB; ABL35775.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS Example 7; Fig 25A-B; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 1238; DB 5; Length 243;
Best Local Similarity 100.0%; Pred. No. 5e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
```

Search completed: March 16, 2006, 20:04:37
Job time : 194 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 16, 2006, 20:01:37 ; Search time 40 Seconds
(without alignments)
548.436 Million cell updates/sec

Title: US-10-609-217-2
Perfect score: 1238
Sequence: 1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1233	99.6	255	4	S31866	Ig gamma-1 chain C
2	1233	99.6	330	1	GHHU	Ig gamma-1 chain C
3	1227	99.1	374	2	S69339	Ig heavy chain V r
4	1180	95.3	234	2	PT0207	Ig gamma chain C r
5	1146	92.6	377	2	A23511	Ig gamma-3 chain C
6	1144	92.4	377	2	A60764	Ig gamma-3 chain C
7	1142.5	92.3	326	1	G2HU	Ig gamma-2 chain C
8	1135	91.7	327	1	G4HU	Ig gamma-4 chain C
9	1121	90.5	289	1	G3HUWI	Ig gamma-3 heavy c
10	918.5	74.2	323	1	GHRB	Ig gamma chain C r
11	906.5	73.2	328	2	I47160	Ig gamma 2b chain
12	906.5	73.2	328	2	I47159	Ig gamma 2a chain
13	903.5	73.0	277	2	I47162	Ig gamma 4 chain c
14	889	71.8	329	1	G2GP	Ig gamma-2 chain C
15	885.5	71.5	328	2	I47158	Ig gamma 1 chain c
16	878.5	71.0	328	2	I47161	Ig gamma 3 chain c
17	855.5	69.1	470	2	S22080	Ig heavy chain pre
18	846	68.3	308	2	C30554	Ig heavy chain C r
19	846	68.3	472	2	S31459	Ig gamma-1 chain -
20	845.5	68.3	329	1	G3MSC	Ig gamma-3 chain C
21	838	67.7	333	2	PS0018	Ig gamma-2b chain
22	834.5	67.4	398	1	G3MSM	Ig gamma-3 chain C
23	827.5	66.8	444	2	PC4436	monoclonal antibod
24	818.5	66.1	326	2	PS0017	Ig gamma-1 chain C
25	817.5	66.0	324	1	G1MS	Ig gamma-1 chain C
26	812.5	65.6	393	1	G1MSM	Ig gamma-1 chain C
27	809.5	65.4	329	2	S00847	Ig gamma-2c chain
28	809	65.3	330	1	G2MSA	Ig gamma-2a chain
29	809	65.3	469	2	S37483	Ig gamma-2a chain
30	804	64.9	399	1	G2MSAM	Ig gamma-2a chain
31	802	64.8	335	1	G2MSAB	Ig gamma-2a chain
32	794	64.1	446	2	S40295	Ig gamma-2a chain
33	785.5	63.4	322	2	PS0019	Ig gamma-2a chain
34	779	62.9	474	1	G2MS11	Ig gamma-2b chain
35	774	62.5	405	1	G2MSBM	Ig gamma-2b chain
36	764	61.7	327	2	S06611	Ig gamma-2 chain C
37	757	61.1	475	2	S01321	Ig gamma-2b chain
38	707	57.1	180	2	I46732	Ig gamma heavy cha
39	577.5	46.6	249	2	S69340	Ig heavy chain VHI
40	574.5	46.4	218	2	A36040	Ig heavy chain V-I
41	571	46.1	152	2	S14236	Ig gamma-1 chain C
42	395.5	31.9	572	2	B46529	Ig Y heavy chain (
43	358	28.9	343	2	S25644	Ig mu chain C regi
44	358	28.9	453	2	S37768	Ig mu chain C regi
45	357.5	28.9	549	2	S04845	Ig heavy chain pre

ALIGNMENTS

RESULT 1
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene products.
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

Query Match 99.6%; Score 1233; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 5.7e-89;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 88

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 148

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 208

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        209 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 255
```

RESULT 2
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA

A;Residues: 1-330 <ELL>
A;Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Cross-references: UNIPARC:UPI000017378D
A;Note: this sequence has the G1m(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid seque
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A;Cross-references: UNIPARC:UPI000017378E
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Cross-references: UNIPARC:UPI000017378F
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Cross-references: UNIPARC:UPI0000173790
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 99.6%; Score 1233; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 7.9e-89;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 163

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 283

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
```

RESULT 3
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 99.1%; Score 1227; DB 2; Length 374;
Best Local Similarity 99.1%; Pred. No. 2.7e-88;
Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 207

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 267
```

```
Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||
Db        268 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 327

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        328 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 374


RESULT 4
PT0207
Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207; MUID:91287716; PMID:2062315
A;Accession: PT0207
A;Molecule type: mRNA
A;Residues: 1-234 <EHR>
A;Cross-references: UNIPARC:UPI0000176F05
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>

  Query Match             95.3%;  Score 1180;  DB 2;  Length 234;
  Best Local Similarity   98.6%;  Pred. No. 7e-85;
  Matches  217;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              | ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         15 DTTHTCPPCAAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 74

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 134

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        135 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYKTTPPVLDS 194

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 221
              |||||||||||||||||||||||||||||||||||||||||
Db        195 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 234


RESULT 5
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cc
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:g33070; PIDN:CAA272
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

  Query Match             92.6%;  Score 1146;  DB 2;  Length 377;
  Best Local Similarity   92.5%;  Pred. No. 5.7e-82;
  Matches  210;  Conservative    8;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |    || ||||||||||||||||||||||||||||||||||||||||||:| ||||
Db        151 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 210

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              |||||||||||||||||||:|||||||||||||||||||||||||||||||||||| |
Db        211 GVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||:|:|||||||||||||||||||||:||||||| ||||:|||
Db        271 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 330

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||:|||||||||||| :||||||||||
Db        331 DGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPGK 377


RESULT 6
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 converte
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI0000176F0B
C;Superfamily: immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

  Query Match             92.4%;  Score 1144;  DB 2;  Length 377;
  Best Local Similarity   92.5%;  Pred. No. 8.2e-82;
  Matches  210;  Conservative    8;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |    || ||||||||||||||||||||||||||||||||||||||||||:| ||||
Db        151 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 210

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              |||||||||||||||||||:|||||||||||||||||||||||||||||||||||| |
Db        211 GVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||:|:|||||||||||||||||||||:||||||| ||||:|||
Db        271 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 330

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||:|||||||:|||||||||||| :||||||||||
Db        331 DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNRFTQKSLSLSPGK 377


RESULT 7
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:g32
```

```
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Cross-references: UNIPARC:UPI0000173791
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A;Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
A;Cross-references: UNIPARC:UPI0000173794
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             92.3%;  Score 1142.5;  DB 1;  Length 326;
  Best Local Similarity   94.1%;  Pred. No. 8.9e-82;
  Matches  209;  Conservative    8;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
              |||||||  : |||||||||||||||||||||||||||||||||||:||||||||||
Db        106 CPPCPAPP-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVH 164

Qy         67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
              ||||||||||:|||:||||||||:|||||||||||||||| |||||||||| ||||||
Db        165 NAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPRE 224

Qy        127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 186
              ||||||||||:|:|||||||||||||||||||||||||||||||||||||:||||||||
Db        225 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFF 284

Qy        187 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||
Db        285 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326


RESULT 8
G4HU
Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104; PMID:6299662
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant re
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
A;Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             91.7%;  Score 1135;  DB 1;  Length 327;
  Best Local Similarity   93.7%;  Pred. No. 3.4e-81;
  Matches  208;  Conservative    8;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
              || ||||| |||||||||||||||||||||||||||||||||| ||||||:||||||||||
Db        106 CPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH 165

Qy         67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
              ||||||||||:|||||||||||||||||||||||||||||| ||: ||||||||||||||
Db        166 NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPRE 225

Qy        127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 186
              |||||||||::|:|||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 285

Qy        187 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||:|||||||||:|||||||||||||||||||||||||| ||
Db        286 LYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327


RESULT 9
```

```
G3HUWI
Ig gamma-3 heavy chain disease proteins - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C;Accession: A90442; A92219; A90198; A93915; A02149
R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-
A;Reference number: A90442; MUID:81021548; PMID:6774747
A;Contents: heavy chain disease protein Wis
A;Accession: A90442
A;Molecule type: protein
A;Residues: 1-289 <FRA>
A;Cross-references: UNIPARC:UPI0000173797
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co
A;Note: the sequence of residues 42-76 was taken from the reference that follows
R;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
A;Reference number: A92219; MUID:77118561; PMID:402363
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W
A;Accession: A92219
A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Cross-references: UNIPARC:UPI0000173798
A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
idue segment (12-28)
A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter
R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the
A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
A;Accession: A90198
A;Molecule type: protein
A;Residues: 59-125,'EB',128-226,228-289 <WOL>
A;Cross-references: UNIPARC:UPI0000173799
A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the
R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.;
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion
A;Reference number: A93915; MUID:82247835; PMID:6808505
A;Contents: heavy chain disease protein Omm
A;Accession: A93915
A;Molecule type: mRNA
A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157
A;Cross-references: UNIPARC:UPI000017379A; UNIPARC:UPI000017379B; UNIPARC:UPI000017379C;
A;Note: a carboxyl-terminal Lys is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain subclass
C;Comment: The heavy chain disease protein Wis is shown.
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F;203-270/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             90.5%;  Score 1121;  DB 1;  Length 289;
  Best Local Similarity   90.3%;  Pred. No. 3.6e-80;
  Matches  204;  Conservative   13;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |    || |||||||||||||||||||||||||||||||||||||||||||||||:| ||||
Db         64 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD 123

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||:|||||||||:|:|||:|||||||||||:||:|||||||||||||||||||||| |
Db        124 GVQVHNAKTKPREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTK 183

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              |||||||||||||:|:|||||||||||||||||||||||:||||||| ||||:|||
Db        184 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 243

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 227
              ||||||||||||||||||:|||||||||||| :||||||||||
Db        244 DGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG 289


RESULT 10
GHRB
Ig gamma chain C region - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C;Accession: A91749; A90290; A93928; A90245; A94416; A02161
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot
A;Reference number: A91749; MUID:84030930; PMID:6313520
A;Accession: A91749
A;Molecule type: mRNA
A;Residues: 1-323 <BER>
A;Cross-references: UNIPROT:P01870; UNIPARC:UPI000012B37D
A;Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R;Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob
A;Reference number: A90290; MUID:76135469; PMID:1243651
A;Accession: A90290
A;Molecule type: protein
A;Residues: 1-47,'E',49-71,'PV',72-128 <PRA>
A;Cross-references: UNIPARC:UPI00001737AB
R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
A;Reference number: A93928; MUID:83299917; PMID:6193512
A;Accession: A93928
A;Molecule type: mRNA
A;Residues: 88-103,'M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>
A;Cross-references: UNIPARC:UPI000016C5ED; GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:g
A;Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker
R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin C
A;Reference number: A90245; MUID:70110015; PMID:5461106
A;Accession: A90245
A;Molecule type: protein
A;Residues: 132-143,'E',145-161 <FRU>
A;Cross-references: UNIPARC:UPI00001737AC
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,
A;Reference number: A94416
A;Accession: A94416
A;Molecule type: protein
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',
A;Cross-references: UNIPARC:UPI00001737AD; UNIPARC:UPI00001737AE
A;Note: this has the e15 allotypic marker, 185-Ala
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-82/Domain: immunoglobulin homology <IM1>
F;130-199/Domain: immunoglobulin homology <IM2>
F;236-303/Domain: immunoglobulin homology <IM3>
F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             74.2%;  Score 918.5;  DB 1;  Length 323;
  Best Local Similarity   71.7%;  Pred. No. 2.6e-64;
  Matches  167;  Conservative   29;  Mismatches   32;  Indels    5;  Gaps    2;

Qy          1 MDKT---HTC--PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 55
              :|||     ||  | || ||||||||||:||||||||||||||||||||| :||||:
Db         91 VDKTVAPSTCSKPTCPPPELLGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQ 150
```

```
Qy          56 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 115
               | ||::  :|  |:   ||:|:||| |||| | : ||||| |||:|||| ||||||||||
Db         151 FTWYINNEQVRTARPPLREQQFNSTIRVVSTLPITHQDWLRGKEFKCKVHNKALPAPIEK 210

Qy         116 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 175
               |||||:||| ||:|||: | |:||:   |||||:: ||||||:|||| ||: |:|||||
Db         211 TISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTT 270

Qy         176 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
               | ||||||||:|||:||:|  | ||:|:||:|||||||||||||||:| ||||
Db         271 PAVLDSDGSYFLYNKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK 323


RESULT 11
I47160
Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47160
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: UNIPARC:UPI0000115525; EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PI
C;Genetics:
A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match             73.2%;  Score 906.5;  DB 2;  Length 328;
  Best Local Similarity   73.2%;  Pred. No. 2.3e-63;
  Matches  164;  Conservative   29;  Mismatches   28;  Indels    3;  Gaps    2;

Qy           7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
               || ||| |   |||||:||||||||||||||:||||||| |:|||:|:|||||||||
Db         106 CPICPACE-SPGPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVH 164

Qy          67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
               |:|:|:|||:|||||||||| : |||||||||:||||:|| ||||| : ||||||| ||
Db         165 TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE 224

Qy         127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGS 184
               ||||||||  :||::::||:|||| |||| || |||: |||  || ||:||||  | ||:
Db         225 PQVYTLPPHAEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT 284

Qy         185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
               :||||| :|||: || | :| |:|||||||||||||:| :|||
Db         285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328


RESULT 12
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: UNIPARC:UPI0000115524; EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PI
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match             73.2%;  Score 906.5;  DB 2;  Length 328;
  Best Local Similarity   73.2%;  Pred. No. 2.3e-63;
  Matches  164;  Conservative   29;  Mismatches   28;  Indels    3;  Gaps    2;

Qy           7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
               || ||| |   |||||:||||||||||||||:||||||| |:|||:|:|||||||||
Db         106 CPICPACE-SPGPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVH 164

Qy          67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
               |:|:|:|||:|||||||||| : |||||||||:||||:|| ||||| : ||||||| ||
Db         165 TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE 224

Qy         127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGS 184
               ||||||||  :||::::||:|||| |||| || |||: |||  || ||:||||  | ||:
Db         225 PQVYTLPPHAEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT 284

Qy         185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
               :||||| :|||: || | :| |:|||||||||||||:| :|||
Db         285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328


RESULT 13
I47162
Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47162
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
A;Cross-references: UNIPARC:UPI0000115527; EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PI
C;Genetics:
A;Gene: IgG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>

  Query Match             73.0%;  Score 903.5;  DB 2;  Length 277;
  Best Local Similarity   71.1%;  Pred. No. 3.2e-63;
  Matches  167;  Conservative   30;  Mismatches   31;  Indels    7;  Gaps    4;

Qy           1 MDK---THTCPPCP-APELLG-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 55
               :||   | | ||||  |   | ||| |:|||||||||||||:|||||||| |:|||:
Db          43 VDKRVGTKTKPPCPICPACEGPGPSAFIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQ 102

Qy          56 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 115
               |:|||||||| |:|:|:|||:|||||||| : |||||||||:||||:|| ||||| :
Db         103 FSWYVDGVEVHTAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITR 162

Qy         116 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYK 173
               ||||||| ||||||||||  :||::::|:||||| |||| || |||: |||  || ||:
Db         163 IISKAKGQTREPQVYTLPPPTEELSRSKVTLTCLVTGFYPPDIDVEWQRNGQPEPEGNYR 222

Qy         174 TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
               |||| | ||::|||||| ||| ||:|: | |:|||||||||||||:  :|||
Db         223 TTPPQQDVDGTYFLYSKLAVDKASWQRGDTFQCAVMHEALHNHYTQKSIFKTPGK 277


RESULT 14
G2GP
Ig gamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
C;Accession: A94553; A90352; A90359; A90384; A90385; A02151
R;Trischmann, T.M.
submitted to the Atlas, April 1975
A;Reference number: A94553
```

```
A;Accession: A94553
A;Molecule type: protein
A;Residues: 1-3 <TRI>
A;Cross-references: UNIPROT:P01862; UNIPARC:UPI0000017379E
R;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
A;Reference number: A90352; MUID:71058471; PMID:5538606
A;Accession: A90352
A;Molecule type: protein
A;Residues: 4-68 <BIR>
A;Cross-references: UNIPARC:UPI0000017379F
R;Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Ami
A;Reference number: A90359; MUID:71058486; PMID:5538616
A;Accession: A90359
A;Molecule type: protein
A;Residues: 69-133;312-329 <TUR>
A;Cross-references: UNIPARC:UPI00001737A0; UNIPARC:UPI00001737A1
R;Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90384; MUID:75036072; PMID:4429665
A;Accession: A90384
A;Molecule type: protein
A;Residues: 134-226 <TRA>
A;Cross-references: UNIPARC:UPI00001737A2
R;Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90385; MUID:75036073; PMID:4609467
A;Accession: A90385
A;Molecule type: protein
A;Residues: 227-311 <TR2>
A;Cross-references: UNIPARC:UPI00001737A3
R;Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A;Reference number: A90354; MUID:71058474; PMID:4922544
A;Contents: annotation; disulfide bonds
A;Note: Cys-16 is involved in a heavy-light chain bond
A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;21-81/Domain: immunoglobulin homology <IM1>
F;135-204/Domain: immunoglobulin homology <IM2>
F;241-310/Domain: immunoglobulin homology <IM3>
F;28-79/Disulfide bonds: #status experimental
F;142-202/Disulfide bonds: #status experimental
F;178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;248-308/Disulfide bonds: #status experimental

  Query Match            71.8%;  Score 889;  DB 1;  Length 329;
  Best Local Similarity  72.3%;  Pred. No. 5.3e-62;
  Matches  162;  Conservative   24;  Mismatches   36;  Indels    2;  Gaps    1;

Qy          6 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 65
              ||| || || |||||||:|||||||||||| || ||||||||| ::|||:| |:||    |
Db        106 TCPKCPPPENLGGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPV 165

Qy         66 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125
               ||:|||| ||||:|:|| ||| : ||||| |||:|||| |||||||||||||| || ||
Db        166 GNAETKPRVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPR 225

Qy        126 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDG 183
               | |||||||||||:|::||:|||:  |:|:|| ||| ||  |  |  || |||: |:||
Db        226 MPDVYTLPPSRDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKNTPPIEDADG 285

Qy        184 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 227
```

```
              |:|||||||||||| | || |::|||||||||||| |||::| |||
Db        286 SYFLYSKLTVDKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329


RESULT 15
I47158
Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: UNIPARC:UPI0000115523; EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PI
C;Genetics:
A;Gene: IgG1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match            71.5%;  Score 885.5;  DB 2;  Length 328;
  Best Local Similarity  72.4%;  Pred. No. 1e-61;
  Matches  163;  Conservative   27;  Mismatches   32;  Indels    3;  Gaps    2;

Qy          6 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 65
              ||| ||  | : |||||:||||||||||||:|||||||||||| |  ||:|:|||||||
Db        105 TCPICPGCE-VAGPSVFIFPPKPKDTLMISQTPEVTCVVVDVSKEHAEVQFSWYVDGVEV 163

Qy         66 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125
               | |:|:|:|||:|||||||||| : ||||| |||:||||:|  ||||| :||||| || |
Db        164 HTAETRPKEEQFNSTYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSR 223

Qy        126 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDG 183
               |||||||||  :||:::|:||||| |||| || |||:|||  ||| |:|||  | ||
Db        224 EPQVYTLPPPAEELSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPPQQDVDG 283

Qy        184 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
               :||||||| |||:||  |: | |:|||||||||||||:| : ||
Db        284 TFFLYSKLAVDKARWDHGDKFECAVMHEALHNHYTQKSISKTQGK 328


Search completed: March 16, 2006, 20:05:20
Job time : 41 secs
```

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup)** that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

OM protein - protein search, using sw model

Run on: March 16, 2006, 19:57:23 ; Search time 228 Seconds
(without alignments)
705.528 Million cell updates/sec

Title: US-10-609-217-2
Perfect score: 1238
Sequence: 1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1233	99.6	330	1	IGHG1_HUMAN	P01857 homo sapien
2	1233	99.6	465	2	Q6GMX6_HUMAN	Q6gmx6 homo sapien
3	1233	99.6	466	2	Q6IN78_HUMAN	Q6in78 homo sapien
4	1233	99.6	469	2	Q569F4_HUMAN	Q569f4 homo sapien
5	1233	99.6	469	2	Q7Z7P5_HUMAN	Q7z7p5 homo sapien
6	1233	99.6	470	2	Q7Z5W1_HUMAN	Q7z5w1 homo sapien
7	1233	99.6	470	2	Q6PJA4_HUMAN	Q6pja4 homo sapien
8	1233	99.6	472	2	Q6N089_HUMAN	Q6n089 homo sapien
9	1233	99.6	475	2	Q5EFE5_HUMAN	Q5efe5 homo sapien
10	1233	99.6	475	2	Q6GMW7_HUMAN	Q6gmw7 homo sapien
11	1233	99.6	476	2	Q6GMX1_HUMAN	Q6gmx1 homo sapien
12	1233	99.6	679	2	Q96PQ8_HUMAN	Q96pq8 homo sapien
13	1229	99.3	473	2	Q6P055_HUMAN	Q6p055 homo sapien
14	1229	99.3	475	2	Q6MZQ6_HUMAN	Q6mzq6 homo sapien
15	1229	99.3	480	2	Q6N094_HUMAN	Q6n094 homo sapien
16	1229	99.3	481	2	Q6N097_HUMAN	Q6n097 homo sapien
17	1229	99.3	482	2	Q7Z351_HUMAN	Q7z351 homo sapien
18	1227	99.1	348	2	Q6PYX1_HUMAN	Q6pyx1 homo sapien
19	1227	99.1	473	2	Q6MZV7_HUMAN	Q6mzv7 homo sapien
20	1227	99.1	478	2	Q6PI81_HUMAN	Q6pi81 homo sapien
21	1227	99.1	480	2	Q6PJF1_HUMAN	Q6pjf1 homo sapien
22	1226	99.0	466	2	Q6N096_HUMAN	Q6n096 homo sapien
23	1222	98.7	475	2	Q6N095_HUMAN	Q6n095 homo sapien
24	1222	98.7	544	2	Q6PJ95_HUMAN	Q6pj95 homo sapien
25	1216	98.2	487	2	Q65ZL2_9MURI	Q65zl2 mus sp. fv/
26	1172	94.7	475	2	Q5RE17_PONPY	Q5re17 pongo pygma
27	1146	92.6	354	2	Q86TT2_HUMAN	Q86tt2 homo sapien
28	1146	92.6	518	2	Q6N030_HUMAN	Q6n030 homo sapien
29	1146	92.6	519	2	Q5EBM2_HUMAN	Q5ebm2 homo sapien
30	1142.5	92.3	326	1	IGHG2_HUMAN	P01859 homo sapien
31	1142.5	92.3	417	2	Q6N093_HUMAN	Q6n093 homo sapien
32	1142	92.2	521	2	Q8N4Y9_HUMAN	Q8n4y9 homo sapien
33	1139.5	92.0	464	2	Q6MZU6_HUMAN	Q6mzu6 homo sapien
34	1137.5	91.9	465	2	Q6P6C4_HUMAN	Q6p6c4 homo sapien
35	1135	91.7	327	1	IGHG4_HUMAN	P01861 homo sapien
36	1135	91.7	473	2	Q8TC63_HUMAN	Q8tc63 homo sapien
37	1131	91.4	509	2	Q8NF17_HUMAN	Q8nf17 homo sapien
38	1128.5	91.2	470	2	Q68CN4_HUMAN	Q68cn4 homo sapien
39	1126	91.0	290	1	IGHG3_HUMAN	P01860 homo sapien
40	1126	91.0	476	2	Q6MZX7_HUMAN	Q6mzx7 homo sapien
41	918.5	74.2	323	1	GC_RABIT	P01870 oryctolagus
42	909	73.4	337	2	Q95M34_HORSE	Q95m34 equus cabal
43	889	71.8	329	1	IGHG2_CAVPO	P01862 cavia porce
44	845.5	68.3	329	1	GC3_MOUSE	P22436 mus musculu
45	845.5	68.3	470	2	Q7TMK1_MOUSE	Q7tmk1 mus musculu

ALIGNMENTS

RESULT 1
IGHG1_HUMAN
ID IGHG1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig gamma-1 chain C region.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP PROTEIN SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT peptides of the H-chain, alignment of the tryptic peptides and
RT discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.

```
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT   characterization of the protein, the L- and H-chains, the cyanogen
RT   bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=81208100; PubMed=7236608;
RA   Deisenhofer J.;
RT   "Crystallographic refinement and atomic models of a human Fc fragment
RT   and its complex with fragment B of protein A from Staphylococcus
RT   aureus at 2.9- and 2.8-A resolution.";
RL   Biochemistry 20:2361-2370(1981).
CC   -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
CC       G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC       G1M(3) marker and the G1M (non-1) markers.
CC   -!- MISCELLANEOUS: Nie also differs in the amidation states of 35,
CC       116, 198, 269 and 272.
CC   -!- MISCELLANEOUS: EU also differs in the amidation states of residues
CC       155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC       268-272.
CC   -!- MISCELLANEOUS: KOL also differs in the amidation states of
CC       residues 198, 267 and 272.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; J00228; AAC82527.1; ALT_INIT; Genomic_DNA.
DR   PIR; A93433; GHHU.
DR   PDB; 1AJ7; X-ray; H=1-103.
DR   PDB; 1AQK; X-ray; H=1-103.
DR   PDB; 1D5B; X-ray; B/H=1-101.
DR   PDB; 1D5I; X-ray; H=1-101.
DR   PDB; 1D6V; X-ray; H=1-101.
DR   PDB; 1DN2; X-ray; A/B=120-326.
DR   PDB; 1E4K; X-ray; A/B=106-330.
DR   PDB; 1FC1; X-ray; A/B=106-329.
DR   PDB; 1FC2; X-ray; D=106-329.
DR   PDB; 1FCC; X-ray; A=121-326.
DR   PDB; 1HZH; X-ray; H/K=1-330.
DR   PDB; 1I7Z; X-ray; B/D=1-103.
DR   PDB; 1IIS; X-ray; A/B=107-330.
DR   PDB; 1IIX; X-ray; A/B=107-330.
DR   PDB; 1L6X; X-ray; A=120-326.
DR   PDB; 1OQX; X-ray; A/B=119-330.
DR   PDB; 1T83; X-ray; A/B=107-330.
DR   PDB; 2RCS; X-ray; H=1-103.
DR   HGNC; HGNC:5525; IGHG1.
DR   MIM; 147100; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF07654; C1-set; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   3D-structure; Direct protein sequencing; Glycoprotein;
KW   Immunoglobulin C region; Immunoglobulin domain.
FT   REGION        1     98       CH1.
FT   REGION       99    110       Hinge.
FT   REGION      111    223       CH2.
FT   REGION      224    330       CH3.
FT   CARBOHYD    180    180       N-linked (GlcNAc. . .).
FT   DISULFID     27     83
FT   DISULFID    103    103       Interchain (with light chain).
FT   DISULFID    109    109       Interchain (with heavy chain).
FT   DISULFID    112    112       Interchain (with heavy chain).
FT   DISULFID    144    204
FT   DISULFID    250    308
FT   VARIANT      97     97       K -> R (in G1M(3) marker).
FT                                /FTId=VAR_003886.
FT   VARIANT     239    239       D -> E (in G1M(non-1) marker).
FT                                /FTId=VAR_003887.
FT   VARIANT     241    241       L -> M (in G1M(non-1) marker).
FT                                /FTId=VAR_003888.
FT   NON_TER       1      1
FT   STRAND       23     24
FT   STRAND       26     33
FT   STRAND       38     38
FT   STRAND       41     41
FT   TURN         42     45
FT   TURN         48     49
FT   STRAND       50     52
FT   STRAND       57     58
FT   TURN         59     61
FT   STRAND       62     71
FT   HELIX        73     75
FT   TURN         76     78
FT   STRAND       82     87
FT   TURN         88     91
FT   STRAND       92     97
FT   TURN        102    103
FT   STRAND      122    126
FT   HELIX       130    134
FT   TURN        136    137
FT   STRAND      141    149
FT   STRAND      157    162
FT   TURN        163    164
FT   STRAND      165    167
FT   STRAND      171    172
FT   STRAND      176    177
FT   TURN        179    180
FT   STRAND      183    190
FT   HELIX       193    197
FT   TURN        198    199
FT   STRAND      202    207
FT   TURN        209    210
FT   STRAND      215    219
FT   STRAND      227    227
FT   STRAND      230    234
FT   HELIX       238    242
FT   STRAND      245    256
FT   STRAND      261    266
FT   TURN        267    268
FT   STRAND      269    270
FT   STRAND      274    276
FT   STRAND      280    281
FT   TURN        283    284
FT   STRAND      287    296
FT   HELIX       297    301
FT   TURN        302    303
FT   STRAND      306    311
FT   TURN        313    314
FT   HELIX       316    318
FT   STRAND      319    324
SQ   SEQUENCE   330 AA;  36106 MW;  3770EE106C2FA33D CRC64;

  Query Match             99.6%;  Score 1233;  DB 1;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-92;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 163

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 283

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                 ||||||||||||||||||||||||||||||||||||||||||||||
Db        284 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 2
Q6GMX6_HUMAN
ID   Q6GMX6_HUMAN PRELIMINARY;      PRT;   465 AA.
AC   Q6GMX6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073766; AAH73766.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA;  51083 MW;  B3A9B7D0FDB1386E CRC64;

  Query Match             99.6%;  Score 1233;  DB 2;  Length 465;
  Best Local Similarity   100.0%;  Pred. No. 9e-92;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 298

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 358

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 418

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                 ||||||||||||||||||||||||||||||||||||||||||||||
Db        419 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 465


RESULT 3
Q6IN78_HUMAN
ID   Q6IN78_HUMAN PRELIMINARY;      PRT;   466 AA.
AC   Q6IN78;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGHG1 protein.
GN   Name=IGHG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral Nervous System;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral Nervous System;
RG   NIH MGC Project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC072419; AAH72419.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
```

```
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   466 AA;  50854 MW;  53EB0BCEDE81076E CRC64;

  Query Match             99.6%;  Score 1233;  DB 2;  Length 466;
  Best Local Similarity   100.0%;  Pred. No. 9e-92;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 299

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 359

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 419

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 466


RESULT 4
Q569F4_HUMAN
ID   Q569F4_HUMAN PRELIMINARY;      PRT;   469 AA.
AC   Q569F4;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   IGHG1 protein.
GN   Name=IGHG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lymph;
RG   NIH MGC Project;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC092518; AAH92518.1; -; mRNA.
SQ   SEQUENCE   469 AA;  51254 MW;  AC13448E3047784F CRC64;

  Query Match             99.6%;  Score 1233;  DB 2;  Length 469;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-92;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 302

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 362

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 422

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 469


RESULT 5
Q7Z7P5_HUMAN
ID   Q7Z7P5_HUMAN PRELIMINARY;      PRT;   469 AA.
AC   Q7Z7P5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHG1 protein.
GN   Name=IGHG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RG   NIH MGC Project;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC051328; AAH51328.1; -; mRNA.
DR   HSSP; P01857; 1HZH.
DR   SMR; Q7Z7P5; 20-469.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
```

```
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   469 AA;  51395 MW;  C8D5BE12BAAF795C CRC64;

  Query Match           99.6%;  Score 1233;  DB 2;  Length 469;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-92;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 302

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 362

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 422

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 469


RESULT 6
Q7Z5W1_HUMAN
ID   Q7Z5W1_HUMAN PRELIMINARY;      PRT;   470 AA.
AC   Q7Z5W1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053984; AAH53984.1; -; mRNA.
DR   HSSP; P01857; 1HZH.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein; Immunoglobulin domain.
SQ   SEQUENCE   470 AA;  51204 MW;  778CF34521483E1A CRC64;

  Query Match           99.6%;  Score 1233;  DB 2;  Length 470;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-92;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 303

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 363

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 423

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 7
Q6PJA4_HUMAN
ID   Q6PJA4_HUMAN PRELIMINARY;      PRT;   470 AA.
AC   Q6PJA4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGHG1 protein.
GN   Name=IGHG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RG   NIH MGC Project;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
```

```
DR   EMBL; BC018747; AAH18747.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   SMR; Q6PJA4; 20-470.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   470 AA;  51716 MW;  7B49556A11FD7D99 CRC64;

  Query Match             99.6%;  Score 1233;  DB 2;  Length 470;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-92;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 303

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 363

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 423

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        424 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 8
Q6N089_HUMAN
ID   Q6N089_HUMAN PRELIMINARY;      PRT;   472 AA.
AC   Q6N089;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686P15220.
GN   Name=DKFZp686P15220;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Rectum tumor;
RG   The German cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640627; CAE45781.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA;  51724 MW;  26CB340D0046D279 CRC64;

  Query Match             99.6%;  Score 1233;  DB 2;  Length 472;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-92;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 305

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 365

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 425

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        426 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 472


RESULT 9
Q5EFE5_HUMAN
ID   Q5EFE5_HUMAN PRELIMINARY;      PRT;   475 AA.
AC   Q5EFE5;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Anti-RhD monoclonal T125 gamma1 heavy chain precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Gaucher C., Klein P., Beliard R.;
RT   "Sequence determination of the recombinant human anti-RhD monoclonal
RT   antibody T125.";
RL   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY894992; AAW82028.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF07686; V-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Signal.
FT   SIGNAL       1     19       Potential.
FT   CHAIN       20    475       anti-RhD monoclonal T125 gamma1 heavy
FT                               chain.
SQ   SEQUENCE   475 AA;  52362 MW;  1367D400DC7D2859 CRC64;

  Query Match             99.6%;  Score 1233;  DB 2;  Length 475;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-92;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 308

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 368

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 428

Qy        182 DGSPFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                 ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 DGSPFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475


RESULT 10
Q6GMW7_HUMAN
ID   Q6GMW7_HUMAN PRELIMINARY;      PRT;   475 AA.
AC   Q6GMW7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073782; AAH73782.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   475 AA;  51987 MW;  2A1FE55D736860F8 CRC64;

  Query Match           99.6%;  Score 1233;  DB 2;  Length 475;
  Best Local Similarity  100.0%;  Pred. No. 9.3e-92;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 308

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 368

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 428

Qy        182 DGSPFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                 ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 DGSPFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475


RESULT 11
Q6GMX1_HUMAN
ID   Q6GMX1_HUMAN PRELIMINARY;      PRT;   476 AA.
AC   Q6GMX1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073773; AAH73773.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   476 AA;  52286 MW;  622AABA5C62DDB9D CRC64;

  Query Match           99.6%;  Score 1233;  DB 2;  Length 476;
```

```
  Best Local Similarity   100.0%;  Pred. No. 9.3e-92;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 309

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 369

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 429

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        430 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476


RESULT 12
Q96PQ8_HUMAN
ID   Q96PQ8_HUMAN PRELIMINARY;      PRT;   679 AA.
AC   Q96PQ8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Factor VII active site mutant immunoconjugate.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
RA   Hu Z., Garen A.;
RT   "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT   cells for immunotherapy in mouse models of prostatic cancer.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Hu Z., Garen A.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF272774; AAK58686.2; -; mRNA.
DR   HSSP; P08709; 1KLI.
DR   SMR; Q96PQ8; 39-180, 191-444, 447-679.
DR   Ensembl; ENSG00000057593; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR000152; Asx_hydroxyl_S.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR001438; EGF_II.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002383; GLA_blood.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001254; Peptidase_S1_S6.
DR   InterPro; IPR000294; VitK_dep_GLA.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00008; EGF; 1.
DR   Pfam; PF00594; Gla; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00010; EGFBLOOD.
DR   PRINTS; PR00001; GLABLOOD.
DR   SMART; SM00179; EGF_CA; 1.
DR   SMART; SM00069; GLA; 1.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS50026; EGF_3; 1.
DR   PROSITE; PS01187; EGF_CA; 1.
DR   PROSITE; PS00011; GLA_1; UNKNOWN_1.
DR   PROSITE; PS50998; GLA_2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
SQ   SEQUENCE   679 AA;  75552 MW;  0B0023AE70A067A1 CRC64;

  Query Match             99.6%;  Score 1233;  DB 2;  Length 679;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-91;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 512

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 572

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 632

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        633 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 679


RESULT 13
Q6P055_HUMAN
ID   Q6P055_HUMAN PRELIMINARY;      PRT;   473 AA.
AC   Q6P055;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral Nervous System;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.;
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
```

```
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral Nervous System;
RA   Strausberg R.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC065820; AAH65820.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  51344 MW;  9816D56A77129B57 CRC64;

  Query Match            99.3%;  Score 1229;  DB 2;  Length 473;
  Best Local Similarity  99.6%;  Pred. No. 1.9e-91;
  Matches  226;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 306

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 366

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 426

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||| ||||||||||||||||
Db        427 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 473


RESULT 14
Q6MZQ6_HUMAN
ID   Q6MZQ6_HUMAN PRELIMINARY;      PRT;   475 AA.
AC   Q6MZQ6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686G11190.
GN   Name=DKFZp686G11190;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Esophagus tumor;
RG   The German cDNA Consortium;
RA   Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA   Han M., Wiemann S.;
RL   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640947; CAE45972.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   SMR; Q6MZQ6; 20-475.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   475 AA;  52043 MW;  B7EAE255A26F4B8E CRC64;

  Query Match            99.3%;  Score 1229;  DB 2;  Length 475;
  Best Local Similarity  99.6%;  Pred. No. 2e-91;
  Matches  226;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 308

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 368

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 428

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||| ||||||||||||||||
Db        429 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 475


RESULT 15
Q6N094_HUMAN
ID   Q6N094_HUMAN PRELIMINARY;      PRT;   480 AA.
AC   Q6N094;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686O01196.
GN   Name=DKFZp686O01196;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Esophagus tumor;
RG   The German cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640622; CAE45776.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   480 AA;  52612 MW;  225247F3D35AEC18 CRC64;

  Query Match            99.3%;  Score 1229;  DB 2;  Length 480;
  Best Local Similarity  99.6%;  Pred. No. 2e-91;
  Matches  226;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        254 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 313

Qy         62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 373

Qy        122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 433

Qy        182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
              |||||||||||||||||||||||||||| ||||||||||||||||
Db        434 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 480
```

Search completed: March 16, 2006, 20:01:20
Job time : 231 secs